

**CLAIMS**

Please amend the claims as follows:

1.       **(Currently Amended)**       An isolated small interfering RNA (siRNA) comprising a sequence sufficiently complementary to a portion of an HIV genome to mediate RNA interference (RNAi) of the HIV genome portion, wherein the HIV genome portion is selected from the group consisting of a Long Terminal Repeat (LTR) region, a *nef* gene or portion thereof, and a *vif* gene or portion thereof, and wherein the siRNA promotes the degradation of genomic viral HIV RNA during an early viral replication cycle event to inhibit synthesis of viral reverse-transcription intermediates and establishment of a HIV provirus.
2.       **(Original)**       The siRNA of claim 1, wherein the siRNA is between about 15 and about 25 nucleotides long.
3.       **(Original)**       The siRNA of claim 1, wherein the siRNA is between about 20 and about 23 nucleotides long.
4.       **(Previously Presented)**       The siRNA of claim 1, wherein the HIV genome portion is a Long Terminal Repeat (LTR) region.
5.       **(Previously Presented)**       The siRNA of claim 1, wherein the HIV genome portion is a *nef* gene or portion thereof.
6.       **(Previously Presented)**       The siRNA of claim 1, wherein the HIV genome portion is a *vif* gene or portion thereof.
- 7.-8.   **(Cancel)**
9.       **(Original)**       The siRNA of claim 1, wherein the siRNA is an expressed siRNA.

10.     **(Original)**     The siRNA of claim 1, wherein the siRNA is a synthetic siRNA.
11.     **(Original)**     The siRNA of claim 10, wherein the siRNA is a synthetic 21-nucleotide siRNA.
12.     **(Original)**     The siRNA of claim 1, wherein the siRNA is a short hairpin siRNA (shRNA).
- 13.-19.         **(Cancel)**
20.     **(Original)**     The siRNA of claim 1, wherein the siRNA is modified by the substitution of at least one nucleotide with a modified nucleotide.
21.     **(Original)**     The siRNA of claim 1, wherein the siRNA has at least one mismatch when compared to the sequence of the HIV genome.
- 22-74. **(Cancelled)**
- 75.-83. **(Cancel)**
84.     **(Previously Presented)**     The siRNA of claim 9, wherein said expressed siRNA is expressed from a vector.
85.     **(Previously Presented)**     The siRNA of claim 84, wherein the siRNA is a shRNA.
86.     **(Previously Presented)**     The siRNA of claim 84, wherein the vector is a plasmid vector.
87.     **(Previously Presented)**     The siRNA of claim 84, wherein the vector is a viral vector.

88.     **(Previously Presented)**     The siRNA of claim 84, wherein the vector expresses a plurality of siRNAs comprising sequences sufficiently complementary to portions of the HIV genome.

89.     **(Previously Presented)**     The siRNA of claim 88, wherein at least one of the siRNAs is a shRNA.

90.     **(Currently Amended)**     The siRNA of claim 88, wherein the plurality of siRNAs comprise sequences sufficiently complementary to staggered portions of the HIV genome portion.

91.     **(Cancel)**

92.     **(Previously Presented)**     The siRNA of claim 88, wherein the plurality of siRNAs comprise at least three sequences sufficiently complementary to one or more highly conserved regions of the HIV genome selected from the group consisting of: a *pol* gene or portion thereof, a *tat* gene or portion thereof, a *vif* gene or portion thereof, and a *nef* gene or portion thereof.

93.     **(Previously Presented)**     The siRNA of claim 88, wherein the plurality of siRNAs comprise at least five sequences sufficiently complementary to one or more regions of the HIV genome selected from the group consisting of: a region coding for reverse transcriptase, a region coding for protease, a *tat* gene, a *rev* gene, and a *vif* gene.

94.     **(Previously Presented)**     The siRNA of claim 88, wherein the plurality of siRNAs comprise sequences sufficiently complementary to one or more regions of the HIV genome selected from the group consisting of: a region coding for reverse transcriptase, a region coding for protease, a *tat* gene, a *rev* gene, a *vif* gene, a *gag* gene, a *vpr* gene, a region coding for an envelope protein, a region coding for a capsid protein, and a LTR region.